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100 years of farming: long-term differences in cropping intensity and N fertilization impact soil microbial community structure

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Introduction

- Microbial biodiversity supports key functions (e.g. N cycling) necessary for sustained productivity in agroecosystems.
- Long-term crop production may select for management-specific communities that actively perform biogeochemical cycling.
- We are studying the cumulative effects of 100 years of wheat production on soil microbial communities (SMC) in a long term soil experiment (LTSE) at Lethbridge, AB.

Objectives

- To determine effects of 100 years of varied cropping intensity (CI) on soil microbial abundance and community structure.
- To study the impact of 45 years of N fertilizer application on soil microbial abundance and community structure.

Materials and Methods

- Rotation ABC at Lethbridge is situated on a Orthic Dark Brown Chernozem (MAP 386mm, MAT 5.7°C). The main plot factor is Rotation and sub-plot factor is fertilizer (five pseudoreplicated transects).
  - Rotation A (RA): continuous wheat (W)
  - Rotation C (RC): (W-W-F) all phases all years. Second year wheat was selected (W-W-F; C1 in 2012) to de-emphasize the short term effects of the fallow phase on microbial abundance.
- N (ammonium nitrate) fertilizer treatments :
  - 0 kg ha^{-1} (-N)
  - 45 kg ha^{-1} (+N)
- Soil sampling occurred post harvest in September 2012. Four 10.0 cm depth cores with 3.75 cm diameter were collected for each replicate point along the transects.
- Microbial phospholipid fatty acids (PLFA) were extracted from 4.0 g of freeze dried soil. Samples were quantified using an internal standard (19:0) and identified using GC-FID and the MIDI ™ system. Microbial abundance data were analyzed using ANOVA in SPSS v.20 and community profiles were subjected to non-metric multidimensional scaling (NMDS) ordination in PCOrd v.5.0.
- Soil pH and inorganic nutrients N, P, K and S were determined by ALS Environmental lab (Saskatoon, Saskatchewan).

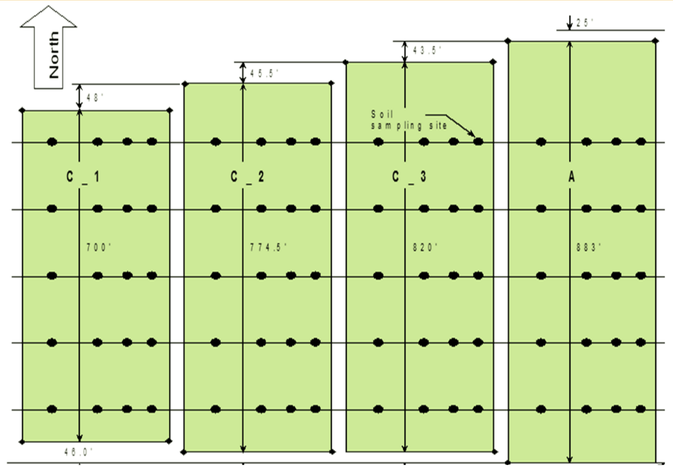

Figure 1: Rotation ABC Plot layout.

Results

Abundance of major soil microbial functional groups

Figure 2: Microbial biomass for RA and RC with +/- N.

- *Total biomass was affected by the interaction of fertilizer with rotation (p<0.02). This pattern is echoed in the bacterial and fungal markers, however no significant interactions were detected.*
- *Both bacterial (p<0.01) and fungal (p<0.02) biomass were higher in fertilized than unfertilized soils.*

Table 1: Quantities of gram positive (Gr+), gram negative (Gr-) bacteria, arbuscular mycorrhizal fungi (AMF) and stress PLFA markers.

	Fertilizer	Gr+	Gr-	AMF	Stress 1	Stress 2
		nmol PLFA g^{-1} soil				
Rotation A	-N	2.5(0.4)	4.3(0.7)	0.8(0.2)	0.4(0.0)	0.3(0.0)
(contin. wheat)	+N	5.5(3.2)	12.0(6.0)	3.8(4.5)	0.4(0.2)	0.3(0.1)
Rotation C	-N	2.4(0.2)	4.0(0.4)	0.8(0.1)	0.4(0.0)	0.2(0.1)
(W-W-F)	+N	3.3(0.7)	5.6(1.8)	1.0(0.2)	0.4(0.0)	0.3(0.1)
ANOVA	R	p<0.18	p<0.06	p<0.22	p<0.99	p<0.46
	F	p<0.03	p<0.01	p<0.17	p<0.91	p<0.10
	RxF	p<0.22	p<0.08	p<0.26	p<0.55	p<0.88

- *Nitrogen fertilizer significantly increased the abundance of both Gram positive and Gram negative bacteria.*

Results

Soil microbial community structure

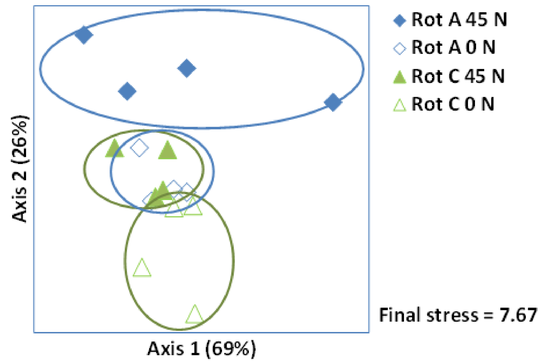

Figure 3: Ordination (NMDS) of microbial PLFA community structure.

- *Microbial community structure was most distinct in the fertilized continuous wheat, compared to the other treatments.*
- *Unfertilized continuous wheat and fertilized W-W-F were similar.*

Table 3: General soil characteristics at the time of sampling (fall 2012).

	Fertilizer	pH	N	P	K	S
			mg kg^{-1} soil			
Rotation A	-N	7.5 (0.1)	4.0 (1.4)	3.3 (1.0)	476 (51)	41.8 (35.1)
(contin. wheat)	+N	6.7(0.4)	11.3(3.4)	4.4(1.7)	677 (161)	10.9 (2.2)
Rotation C	-N	7.8(0.1)	4.8(0.8)	4.4(0.9)	420 (30)	14.5 (1.6)
(W-W-F)	+N	7.4(0.5)	4.7(0.8)	4.5(0.4)	502 (62)	8.1 (0.8)
ANOVA	R	p<0.01	p<0.01	p<0.20	p<0.03	p<0.11
	F	p<0.01	p<0.01	p<0.26	p<0.01	p<0.06
	RxF	p<0.21	p<0.01	p<0.15	p<0.22	p<0.19

- *Rotation and fertilizer altered both pH and K in the soil.*
- *Available N was influenced by an interaction of rotation with fertilizer.*

Summary

- Abundance of broad microbial functional groups were differently affected by both long-term cropping intensity and N fertilizer.
- PLFA profiles provided an overview of the SMC structure in response to management illustrating that agricultural practices have resulted in divergence of microbial populations that drive biogeochemical cycling in agroecosystems.
- Management changes influenced inorganic N concentration.

Additional work

The abundance of N cycling functional gene abundance will be investigated with real-time PCR. Archived soils, dating back to 1910 will be used to study changes in soil bacterial and fungal diversity over time with 16S rRNA and ITS targeted 454 pyrosequencing.

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